

OIKE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/899,295

DATE: 07/24/2001
TIME: 10:54:05

Input Set : A:\00a033e1.app
Output Set: N:\CRF3\07242001\I899295.raw

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3 <110> APPLICANT: Aventis Pharma Deutschland GmbH
5 <120> TITLE OF INVENTION: Process for identifying modulators of G protein coupled
6 receptors
8 <130> FILE REFERENCE: AVE D-2000/A033 englisch
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/899,295
C--> 11 <141> CURRENT FILING DATE: 2001-07-06
13 <160> NUMBER OF SEQ ID NOS: 10
15 <170> SOFTWARE: PatentIn Ver. 2.1
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18 <211> LENGTH: 1080
19 <212> TYPE: DNA
20 <213> ORGANISM: Mus musculus
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25 aagctgctgc tgcctgggac aggagagagt ggcaagagta cgtttatcaa gcagatgaga 180
26 atcatccatg ggtcaggata ctctgatgaa gataaaaggg gcttcaccaa gctgggtgat 240
27 cagaacatct tcacggccat gcaggccatg atcagagcca tggacacact caagatccca 300
28 tacaagtatg agcacaataa ggctcatgca caattagttc gagaagttga tgtggagaag 360
29 gtgtctgctt ttgagaatcc atatgtagat gcaataaaga gtttatggaa tgatcctgga 420
30 atccaggaat gctatgatag acgacgagaa tatcaattat ctgactctac caaatactat 480
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34 gaaaatgtca cctctatcat gtttctagta gcgcttagtg aatatgatca agttctcgtg 720
35 gagtccagaca atgagaaccg aatggaggaa agcaaggctc tctttagaac aattatcaca 780
36 tacccttggt tccagaactc ctcggttatt ctgttcttaa acaagaaaga tcttctagag 840
37 gagaaaatca tgtattccca tctagtgcac tacttcccag aatatgatgg accccagaga 900
38 gatgccagg cagcccagga attcattctg aagatgttcg tggacctgaa cccagacagt 960
39 gacaaaatta tctactccca cttcacgtgc gccacagaca ccgagaatat ccgctttgtc 1020
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46 <213> ORGANISM: Mus musculus
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55 Lys Arg Asp Ala Arg Arg Glu Leu Lys Leu Leu Leu Gly Thr Gly
56 35 40 45
58 Glu Ser Gly Lys Ser Thr Phe Ile Lys Gln Met Arg Ile Ile His Gly
59 50 55 60
61 Ser Gly Tyr Ser Asp Glu Asp Lys Arg Gly Phe Thr Lys Leu Val Tyr
62 65 70 75 80
64 Gln Asn Ile Phe Thr Ala Met Gln Ala Met Ile Arg Ala Met Asp Thr

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70 Val Arg Glu Val Asp Val Glu Lys Val Ser Ala Phe Glu Asn Pro Tyr
71          115          120          125
73 Val Asp Ala Ile Lys Ser Leu Trp Asn Asp Pro Gly Ile Gln Glu Cys
74          130          135          140
76 Tyr Asp Arg Arg Arg Glu Tyr Gln Leu Ser Asp Ser Thr Lys Tyr Tyr
77 145          150          155          160
79 Leu Asn Asp Leu Asp Arg Val Ala Asp Pro Ala Tyr Leu Pro Thr Gln
80          165          170          175
82 Gln Asp Val Leu Arg Val Arg Val Pro Thr Thr Gly Ile Ile Glu Tyr
83          180          185          190
85 Pro Phe Asp Leu Gln Ser Val Ile Phe Arg Met Val Asp Val Gly Gly
86          195          200          205
88 Gln Arg Ser Glu Arg Arg Lys Trp Ile His Cys Phe Glu Asn Val Thr
89          210          215          220
91 Ser Ile Met Phe Leu Val Ala Leu Ser Glu Tyr Asp Gln Val Leu Val
92 225          230          235          240
94 Glu Ser Asp Asn Glu Asn Arg Met Glu Glu Ser Lys Ala Leu Phe Arg
95          245          250          255
97 Thr Ile Ile Thr Tyr Pro Trp Phe Gln Asn Ser Ser Val Ile Leu Phe
98          260          265          270
100 Leu Asn Lys Lys Asp Leu Leu Glu Glu Lys Ile Met Tyr Ser His Leu
101          275          280          285
103 Val Asp Tyr Phe Pro Glu Tyr Asp Gly Pro Gln Arg Asp Ala Gln Ala
104          290          295          300
106 Ala Arg Glu Phe Ile Leu Lys Met Phe Val Asp Leu Asn Pro Asp Ser
107 305          310          315          320
109 Asp Lys Ile Ile Tyr Ser His Phe Thr Cys Ala Thr Asp Thr Glu Asn
110          325          330          335
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128 acaggagaga gtggcaagag tacgtttatc aagcagatga gaatcatcca tgggtcagga 180
129 tactctgatg aagataaaag gggcttcacc aagctggtgt atcagaacat cttcacggcc 240
130 atgcaggcca tgatcagagc catggacaca ctcaagatcc catacaagta tgagcacaat 300
131 aaggctcatg cacaattagt tcgagaagtt gatgtggaga aggtgtctgc ttttgagaat 360
132 ccatatgtag atgcaataaa gagtttatgg aatgatcctg gaatccagga atgctatgat 420
133 agacgacgag aatatcaatt atctgactct accaaatact atcttaatga cttggaccgc 480
134 gtagctgacc ctgcctacct gcctacgcaa caagatgtgc ttagagttcg agtccccacc 540

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135 acagggatca tcgaataccc ctttgactta caaagtgtca ttttcagaat ggtcgatgta 600
136 gggggccaaa ggtcagagag aagaaaatgg atacactgct ttgaaaatgt cacctctatc 660
137 atgtttctag tagcgcttag tgaatatgat caagttctcg tggagtcaga caatgagaac 720
138 cgaatggagg aaagcaaggc tctctttaga acaattatca catacccctg gttccagaac 780
139 tcctcggtta ttctgttctt aaacaagaaa gatcttctag aggagaaaat catgtattcc 840
140 catctagtcg actacttccc agaatatgat ggaccccaga gagatgccca ggcagcccga 900
141 gaattcattc tgaagatggt cgtggacctg aaccagaca gtgacaaaat tatctactcc 960
142 cacttcacgt gcgccacaga caccgagaat atccgctttg tctttgctgc cgtcaaggac 1020
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147 <211> LENGTH: 353
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155 Asp Glu Ile Glu Arg His Val Arg Arg Asp Lys Arg Asp Ala Arg Arg
156 20 25 30
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159 35 40 45
161 Phe Ile Lys Gln Met Arg Ile Ile His Gly Ser Gly Tyr Ser Asp Glu
162 50 55 60
164 Asp Lys Arg Gly Phe Thr Lys Leu Val Tyr Gln Asn Ile Phe Thr Ala
165 65 70 75 80
167 Met Gln Ala Met Ile Arg Ala Met Asp Thr Leu Lys Ile Pro Tyr Lys
168 85 90 95
170 Tyr Glu His Asn Lys Ala His Ala Gln Leu Val Arg Glu Val Asp Val
171 100 105 110
173 Glu Lys Val Ser Ala Phe Glu Asn Pro Tyr Val Asp Ala Ile Lys Ser
174 115 120 125
176 Leu Trp Asn Asp Pro Gly Ile Gln Glu Cys Tyr Asp Arg Arg Arg Glu
177 130 135 140
179 Tyr Gln Leu Ser Asp Ser Thr Lys Tyr Tyr Leu Asn Asp Leu Asp Arg
180 145 150 155 160
182 Val Ala Asp Pro Ala Tyr Leu Pro Thr Gln Gln Asp Val Leu Arg Val
183 165 170 175
185 Arg Val Pro Thr Gly Ile Ile Glu Tyr Pro Phe Asp Leu Gln Ser
186 180 185 190
188 Val Ile Phe Arg Met Val Asp Val Gly Gly Gln Arg Ser Glu Arg Arg
189 195 200 205
191 Lys Trp Ile His Cys Phe Glu Asn Val Thr Ser Ile Met Phe Leu Val
192 210 215 220
194 Ala Leu Ser Glu Tyr Asp Gln Val Leu Val Glu Ser Asp Asn Glu Asn
195 225 230 235 240
197 Arg Met Glu Glu Ser Lys Ala Leu Phe Arg Thr Ile Ile Thr Tyr Pro
198 245 250 255
200 Trp Phe Gln Asn Ser Ser Val Ile Leu Phe Leu Asn Lys Lys Asp Leu
201 260 265 270
203 Leu Glu Glu Lys Ile Met Tyr Ser His Leu Val Asp Tyr Phe Pro Glu

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204          275          280          285
206 Tyr Asp Gly Pro Gln Arg Asp Ala Gln Ala Ala Arg Glu Phe Ile Leu
207          290          295          300
209 Lys Met Phe Val Asp Leu Asn Pro Asp Ser Asp Lys Ile Ile Tyr Ser
210 305          310          315          320
212 His Phe Thr Cys Ala Thr Asp Thr Glu Asn Ile Arg Phe Val Phe Ala
213          325          330          335
215 Ala Val Lys Asp Thr Ile Leu Gln Leu Asn Leu Lys Glu Cys Gly Leu
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218 Phe
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225 <212> TYPE: DNA
226 <213> ORGANISM: Mus musculus
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231 acaggagaga gtggcaagag tacgtttatc aagcagatga gaatcatcca tgggtcagga 180
232 tactctgatg aagataaaag gggcttcacc aagctggtgt atcagaacat cttcacggcc 240
233 atgcaggcca tgatcagagc catggacaca ctcaagatcc catacaagta tgagcacaat 300
234 aaggctcatg cacaattagt tcgagaagtt gatgtggaga aggtgtctgc ttttgagaat 360
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236 agacgacgag aatatcaatt atctgactct accaaatact atcttaatga cttggaccgc 480
237 gtagctgacc ctgcctacct gcctacgcaa caagatgtgc ttagagtctg agtccccacc 540
238 acagggatca tcgaataccc ctttgactta caaagtgtca ttttcagaat ggtcgatgta 600
239 gggggccaaa ggtcagagag aagaaaatgg atacactgct ttgaaaatgt cacctctatc 660
240 atgtttctag tagcgcttag tgaatatgat caagttctcg tggagtcaga caatgagaac 720
241 cgaatggagg aaagcaaggc tctctttaga acaattatca catacccctg gttccagaac 780
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243 catctagtct actacttccc agaatatgat ggaccccgag gagatgccca ggcagcccga 900
244 gaattcattc tgaagatggt cgtggacctg aaccagaca gtgacaaaat tatctactcc 960
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250 <211> LENGTH: 353
251 <212> TYPE: PRT
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262          35          40          45
264 Phe Ile Lys Gln Met Arg Ile Ile His Gly Ser Gly Tyr Ser Asp Glu
265          50          55          60
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268 65          70          75          80
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273	Tyr Glu His	Asn Lys Ala His Ala	Gln Leu Val Arg Glu	Val Asp Val		
274		100		105		110
276	Glu Lys Val	Ser Ala Phe Glu Asn	Pro Tyr Val Asp Ala	Ile Lys Ser		
277		115		120		125
279	Leu Trp Asn	Asp Pro Gly Ile Gln	Glu Cys Tyr Asp Arg	Arg Arg Glu		
280		130		135		140
282	Tyr Gln Leu	Ser Asp Ser Thr Lys	Tyr Tyr Leu Asn Asp	Leu Asp Arg		
283	145		150		155	160
285	Val Ala Asp	Pro Ala Tyr Leu Pro	Thr Gln Gln Asp Val	Leu Arg Val		
286		165		170		175
288	Arg Val Pro	Thr Thr Gly Ile Ile	Glu Tyr Pro Phe Asp	Leu Gln Ser		
289		180		185		190
291	Val Ile Phe	Arg Met Val Asp Val	Gly Gly Gln Arg Ser	Glu Arg Arg		
292		195		200		205
294	Lys Trp Ile	His Cys Phe Glu Asn	Val Thr Ser Ile Met	Phe Leu Val		
295		210		215		220
297	Ala Leu Ser	Glu Tyr Asp Gln Val	Leu Val Glu Ser Asp	Asn Glu Asn		
298	225		230		235	240
300	Arg Met Glu	Glu Ser Lys Ala Leu	Phe Arg Thr Ile Ile	Thr Tyr Pro		
301		245		250		255
303	Trp Phe Gln	Asn Ser Ser Val Ile	Leu Phe Leu Asn Lys	Lys Asp Leu		
304		260		265		270
306	Leu Glu Glu	Lys Ile Met Tyr Ser	His Leu Val Asp Tyr	Phe Pro Glu		
307		275		280		285
309	Tyr Asp Gly	Pro Gln Arg Asp Ala	Gln Ala Ala Arg Glu	Phe Ile Leu		
310		290		295		300
312	Lys Met Phe	Val Asp Leu Asn Pro	Asp Ser Asp Lys Ile	Ile Tyr Ser		
313	305		310		315	320
315	His Phe Thr	Cys Ala Thr Asp Thr	Glu Asn Ile Arg Phe	Val Phe Ala		
316		325		330		335
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319		340		345		350

321 Phe

326 <210> SEQ ID NO: 7

327 <211> LENGTH: 1062

328 <212> TYPE: DNA

329 <213> ORGANISM: Mus musculus

331 <400> SEQUENCE: 7

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334 acaggagaga gtggcaagag tacgtttatc aagcagatga gaatcatcca tgggtcagga 180
335 tactctgatg aagataaaag gggcttcacc aagctggtgt atcagaacat cttcacggcc 240
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337 aaggctcatg cacaattagt tcgagaagtt gatgtggaga aggtgtctgc ttttgagaat 360
338 ccatatgtag atgcaataaa gagtttatgg aatgacacct gaatccagga atgctatgat 420
339 agacgacgag aatatcaatt atctgactct accaaatact atcttaatga cttggaccgc 480
340 gtagctgacc ctgcctacct gcctacgcaa caagatgtgc ttagagttcg agtccccacc 540
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L:10 M:270 C: Current Application Number differs, Replaced Application Number

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date